

SEQUENCE LISTING

<110> Becker, Kenneth David
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 Tanzi, Rudolph E.
 Bertram, Lars
 Saunders, Aleister J.
 Mullin, Kristina M.
 Sampson, Andrew Johnson
 Blacker, Deborah Lynne

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g a g t g a g a c c	c t a t c t t a c a	a a a a a g a a g a	a g a a g a a g a a	a a c c a t g a c a	g g t g t c t t t a	30420
a g c t g c c c t t	g c t g t t c t g g	g t t c a t g a a g	c a t c t g t g g g	a g g t t g c c c a	t a t g t a a a a t	30480
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a a t t t t t t c t c	a t t c a a a t c c	t g a a t t a g a a	g t t g t t t g g t	a t a a a t a t t g	a a a a t t g t t g	30600
a g g g g a g a a t	t t a t t c a a a g	t t t a a t c a t t	t t g c t t t t a t	c t a t g t t a t a	c t t a g c t a t t	30660
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<210> 469

<211> 720

<212> DNA

<213> Homo sapiens

<220>

<221> allele

<222> 30,57,85,243,250,377,512,531,555,561,672

<223> N is any

<400> 469

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<212> DNA

<213> Homo sapiens

<400> 470

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 <211> 4910
 <212> DNA
 <213> Homo sapiens

<220>
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<400> 471

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Lys Lys Glu Glu Lys Gly Lys Asn Ile Gln Val Val Val Arg Cys Arg	
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Pro Phe Asn Leu Ala Glu Arg Lys Ala Ser Ala His Ser Ile Val Glu	
30 35 40	
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Cys Asp Pro Val Arg Lys Glu Val Ser Val Arg Thr Gly Gly Leu Ala	
45 50 55	
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Asp Lys Ser Ser Arg Lys Thr Tyr Thr Phe Asp Met Val Phe Gly Ala	
60 65 70	
tct act aaa cag att gat gtt tac cga agt gtt gtt tgt cca att ctg	412
Ser Thr Lys Gln Ile Asp Val Tyr Arg Ser Val Val Cys Pro Ile Leu	
75 80 85 90	
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Asp Glu Val Ile Met Gly Tyr Asn Cys Thr Ile Phe Ala Tyr Gly Gln	
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Thr Gly Thr Gly Lys Thr Phe Thr Met Glu Gly Glu Arg Ser Pro Asn	
110 115 120	
gaa gag tat acc tgg gaa gag gat ccc ttg gct ggt ata att cca cgt	556
Glu Glu Tyr Thr Trp Glu Glu Asp Pro Leu Ala Gly Ile Ile Pro Arg	
125 130 135	
acc ctt cat caa att ttt gag aaa ctt act gat aat ggt act gaa ttt	604
Thr Leu His Gln Ile Phe Glu Lys Leu Thr Asp Asn Gly Thr Glu Phe	
140 145 150	
tca gtc aaa gtg tct ctg ttg gag atc tat aat gaa gag ctt ttt gat	652
Ser Val Lys Val Ser Leu Leu Glu Ile Tyr Asn Glu Glu Leu Phe Asp	
155 160 165 170	
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Asp Pro Arg Asn Lys Arg Gly Val Ile Ile Lys Gly Leu Glu Glu Ile	
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aca gta cac aac aag gat gaa gtc tat caa att tta gaa aag ggg gca	796
Thr Val His Asn Lys Asp Glu Val Tyr Gln Ile Leu Glu Lys Gly Ala	
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Ala Lys Arg Thr Thr Ala Ala Thr Leu Met Asn Ala Tyr Ser Ser Arg	
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Ser His Ser Val Phe Ser Val Thr Ile His Met Lys Glu Thr Thr Ile	
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Ala	Gly	Ser	Glu	Asn	Ile	Gly	Arg	Ser	Gly	Ala	Val	Asp	Lys	Arg	Ala	
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Arg	Glu	Ala	Gly	Asn	Ile	Asn	Gln	Ser	Leu	Leu	Thr	Leu	Gly	Arg	Val	
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Ile	Thr	Ala	Leu	Val	Glu	Arg	Thr	Pro	His	Val	Pro	Tyr	Arg	Glu	Ser	
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aaa	cta	act	aga	atc	ctc	cag	gat	tct	ctt	gga	ggg	cgt	aca	aga	aca	1132
Lys	Leu	Thr	Arg	Ile	Leu	Gln	Asp	Ser	Leu	Gly	Gly	Arg	Thr	Arg	Thr	
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Pro	Glu	Val	Asn	Gln	Lys	Leu	Thr	Lys	Lys	Ala	Leu	Ile	Lys	Glu	Tyr	
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Thr	Glu	Glu	Ile	Glu	Arg	Leu	Lys	Arg	Asp	Leu	Ala	Ala	Ala	Arg	Glu	
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Gly	Ala	Val	Glu	Glu	Glu	Leu	Asn	Arg	Val	Thr	Glu	Leu	Phe	Met	Asp	
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Gln	Glu	Leu	Glu	Thr	Thr	Gln	Lys	His	Leu	Gln	Glu	Thr	Lys	Leu	Gln	
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Leu	Val	Lys	Glu	Glu	Tyr	Ile	Thr	Ser	Ala	Leu	Glu	Ser	Thr	Glu	Glu	
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Lys	Leu	His	Asp	Ala	Ala	Ser	Lys	Leu	Leu	Asn	Thr	Val	Glu	Glu	Thr	
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Thr	Lys	Asp	Val	Ser	Gly	Leu	His	Ser	Lys	Leu	Asp	Arg	Lys	Lys	Ala	
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Val Asp Gln His Asn Ala Glu Ala Gln Asp Ile Phe Gly Lys Asn Leu	
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Asn Ser Leu Phe Asn Asn Met Glu Glu Leu Ile Lys Asp Gly Ser Ser	
540 545 550	
aag caa aag gcc atg cta gaa gta cat aag acc tta ttt ggt aat ctg	1852
Lys Gln Lys Ala Met Leu Glu Val His Lys Thr Leu Phe Gly Asn Leu	
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Leu Ser Ser Ser Val Ser Ala Leu Asp Thr Ile Thr Thr Val Ala Leu	
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Gly Ser Leu Thr Ser Ile Pro Glu Asn Val Ser Thr His Val Ser Gln	
590 595 600	
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Ile Phe Asn Met Ile Leu Lys Glu Gln Ser Leu Ala Ala Glu Ser Lys	
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Lys Ile Glu Asp Gln Lys Lys Glu Leu Asp Gly Phe Leu Ser Ile Leu	
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Cys Asn Asn Leu His Glu Leu Gln Glu Asn Thr Ile Cys Ser Leu Val	
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Glu Ser Gln Lys Gln Cys Gly Asn Leu Thr Glu Asp Leu Lys Thr Ile	
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Leu Ser Ser Val Gln Glu Asn Ile Gln Gln Lys Ser Lys Asp Ile Val	
750 755 760	
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Phe Ser Gln Glu Leu Arg Asn Phe Asn Gln Glu Gly Thr Lys Leu Val	
780 785 790	

gaa gaa tct gtg aaa cac tct gat aaa ctc aat ggc aac ctg gaa aaa Glu Glu Ser Val Lys His Ser Asp Lys Leu Asn Gly Asn Leu Glu Lys 795 800 805 810	2572
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<212> PRT

<213> Homo sapiens

<220>

<221> VARIANT

<222> 869

<223> Xaa = any amino acid

<400>, 472

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Arg Lys Ala Ser Ala His Ser Ile Val Glu Cys Asp Pro Val Arg Lys
35      40      45
Glu Val Ser Val Arg Thr Gly Gly Leu Ala Asp Lys Ser Ser Arg Lys
50      55      60
Thr Tyr Thr Phe Asp Met Val Phe Gly Ala Ser Thr Lys Gln Ile Asp
65      70      75      80
Val Tyr Arg Ser Val Val Cys Pro Ile Leu Asp Glu Val Ile Met Gly
85      90      95
Tyr Asn Cys Thr Ile Phe Ala Tyr Gly Gln Thr Gly Thr Gly Lys Thr
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Phe Thr Met Glu Gly Glu Arg Ser Pro Asn Glu Glu Tyr Thr Trp Glu
115     120     125
Glu Asp Pro Leu Ala Gly Ile Ile Pro Arg Thr Leu His Gln Ile Phe
130     135     140
Glu Lys Leu Thr Asp Asn Gly Thr Glu Phe Ser Val Lys Val Ser Leu
145     150     155     160
Leu Glu Ile Tyr Asn Glu Glu Leu Phe Asp Leu Leu Asn Pro Ser Ser
165     170     175
Asp Val Ser Glu Arg Leu Gln Met Phe Asp Asp Pro Arg Asn Lys Arg
180     185     190
Gly Val Ile Ile Lys Gly Leu Glu Glu Ile Thr Val His Asn Lys Asp
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Ala	Thr	Leu	Met	Asn	Ala	Tyr	Ser	Ser	Arg	Ser	His	Ser	Val	Phe	Ser
225					230					235					240
Val	Thr	Ile	His	Met	Lys	Glu	Thr	Thr	Ile	Asp	Gly	Glu	Glu	Leu	Val
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Lys	Ile	Gly	Lys	Leu	Asn	Leu	Val	Asp	Leu	Ala	Gly	Ser	Glu	Asn	Ile
			260					265					270		
Gly	Arg	Ser	Gly	Ala	Val	Asp	Lys	Arg	Ala	Arg	Glu	Ala	Gly	Asn	Ile
		275					280					285			
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Gln	Asp	Ser	Leu	Gly	Gly	Arg	Thr	Arg	Thr	Ser	Ile	Ile	Ala	Thr	Ile
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Ser	Pro	Ala	Ser	Leu	Asn	Leu	Glu	Glu	Thr	Leu	Ser	Thr	Leu	Glu	Tyr
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Ala	His	Arg	Ala	Lys	Asn	Ile	Leu	Asn	Lys	Pro	Glu	Val	Asn	Gln	Lys
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Ser	Glu	Glu	Asn	Phe	Arg	Val	Met	Ser	Gly	Lys	Leu	Thr	Val	Gln	Glu
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Glu	Gln	Ile	Val	Glu	Leu	Ile	Glu	Lys	Ile	Gly	Ala	Val	Glu	Glu	Glu
			420					425					430		
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Gln	Cys	Lys	Ser	Asp	Leu	Gln	Asn	Lys	Thr	Gln	Glu	Leu	Glu	Thr	Thr
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Gln	Lys	His	Leu	Gln	Glu	Thr	Lys	Leu	Gln	Leu	Val	Lys	Glu	Glu	Tyr
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Ile	Thr	Ser	Ala	Leu	Glu	Ser	Thr	Glu	Glu	Lys	Leu	His	Asp	Ala	Ala
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Ser	Lys	Leu	Leu	Asn	Thr	Val	Glu	Glu	Thr	Thr	Lys	Asp	Val	Ser	Gly
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Leu	His	Ser	Lys	Leu	Asp	Arg	Lys	Lys	Ala	Val	Asp	Gln	His	Asn	Ala
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Glu	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Asn	Leu	Asn	Ser	Leu	Phe	Asn	Asn
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Met	Glu	Glu	Leu	Ile	Lys	Asp	Gly	Ser	Ser	Lys	Gln	Lys	Ala	Met	Leu
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Glu	Val	His	Lys	Thr	Leu	Phe	Gly	Asn	Leu	Ser	Ser	Ser	Val	Ser	
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Ala	Leu	Asp	Thr	Ile	Thr	Thr	Val	Ala	Leu	Gly	Ser	Leu	Thr	Ser	Ile
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Pro	Glu	Asn	Val	Ser	Thr	His	Val	Ser	Gln	Ile	Phe	Asn	Met	Ile	Leu
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Lys	Glu	Gln	Ser	Leu	Ala	Ala	Glu	Ser	Lys	Thr	Val	Leu	Gln	Glu	Leu
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Ile	Asn	Val	Leu	Lys	Thr	Asp	Leu	Leu	Ser	Ser	Leu	Glu	Met	Ile	Leu
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Ser	Pro	Thr	Val	Val	Ser	Ile	Leu	Lys	Ile	Asn	Ser	Gln	Leu	Lys	His
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Ile	Phe	Lys	Thr	Ser	Leu	Thr	Val	Ala	Asp	Lys	Ile	Glu	Asp	Gln	Lys
			660					665					670		
Lys	Glu	Leu	Asp	Gly	Phe	Leu	Ser	Ile	Leu	Cys	Asn	Asn	Leu	His	Glu
			675				680					685			
Leu	Gln	Glu	Asn	Thr	Ile	Cys	Ser	Leu	Val	Glu	Ser	Gln	Lys	Gln	Cys
			690			695					700				
Gly	Asn	Leu	Thr	Glu	Asp	Leu	Lys	Thr	Ile	Lys	Gln	Thr	His	Ser	Gln
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Glu	Leu	Cys	Lys	Leu	Met	Asn	Leu	Trp	Thr	Glu	Arg	Phe	Cys	Ala	Leu
				725					730					735	
Glu	Glu	Lys	Cys	Glu	Asn	Ile	Gln	Lys	Pro	Leu	Ser	Ser	Val	Gln	Glu

Asn	Ile	Gln	Lys	Ser	Lys	Asp	Ile	Val	Asn	Lys	Met	Thr	Phe	His	
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Ser	Gln	Lys	Phe	Cys	Ala	Asp	Ser	Asp	Gly	Phe	Ser	Gln	Glu	Leu	Arg
	770					775					780				
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				805						810					815
Gln	Arg	Cys	Glu	Ser	Leu	Asn	Thr	Arg	Thr	Val	Tyr	Phe	Ser	Glu	Gln
			820						825					830	
Trp	Val	Ser	Ser	Leu	Asn	Glu	Arg	Glu	Gln	Glu	Leu	His	Asn	Leu	Leu
			835						840					845	
Glu	Val	Val	Ser	Gln	Cys	Cys	Glu	Ala	Ser	Ser	Ser	Asp	Ile	Thr	Glu
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Lys	Ser	Asp	Gly	Xaa	Lys	Ala	Ala	His	Glu	Lys	Gln	His	Asn	Ile	Phe
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			980					985						990	
Gln	Glu	Pro	Ser	Val	Asp	Ala	Gly	Val	Asp	Cys	Ser	Ser	Ile	Gly	Gly
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Val	Pro	Phe	Phe	Gln	His	Lys	Lys	Ser	His	Gly	Lys	Asp	Lys	Glu	Asn
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Arg	Gly	Ile	Asn	Thr	Leu	Glu	Arg	Ser	Lys	Val	Glu	Glu	Thr	Thr	Glu
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<212> DNA

<213> Homo sapiens

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<221> CDS

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Glu Arg Lys Ala Ser Ala His Ser Ile Val Glu Cys Asp Pro Val Arg
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aaa gaa gtt agt gta cga act gga gga ttg gct gac aag agc tca agg 194
Lys Glu Val Ser Val Arg Thr Gly Gly Leu Ala Asp Lys Ser Ser Arg
50 55 60

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Lys Thr Tyr Thr Phe Asp Met Val Phe Gly Ala Ser Thr Lys Gln Ile	
65 70 75	
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Asp Val Tyr Arg Ser Val Val Cys Pro Ile Leu Asp Glu Val Ile Met	
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Gly Tyr Asn Cys Thr Ile Phe Ala Tyr Gly Gln Thr Gly Thr Gly Lys	
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Thr Phe Thr Met Glu Gly Glu Arg Ser Pro Asn Glu Glu Tyr Thr Trp	
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305 310 315	
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tat gct cat aga gca aag aac ata ttg aat aag cct gaa gtg aat cag Tyr Ala His Arg Ala Lys Asn Ile Leu Asn Lys Pro Glu Val Asn Gln	355	360	365	1106
aaa ctc acc aaa aaa gct ctt att aag gag tat acg gag gag ata gaa Lys Leu Thr Lys Lys Ala Leu Ile Lys Glu Tyr Thr Glu Glu Ile Glu	370	375	380	1154
cgt tta aaa cga gat ctt gct gca gcc cgt gag aaa aat gga gtg tat Arg Leu Lys Arg Asp Leu Ala Ala Ala Arg Glu Lys Asn Gly Val Tyr	385	390	395	1202
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gaa gag cag att gta gaa ttg att gaa aaa att ggt gct gtt gag gag Glu Glu Gln Ile Val Glu Leu Ile Glu Lys Ile Gly Ala Val Glu Glu	420	425	430	1298
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gac cag tgt aaa tct gac ctg caa aat aaa aca caa gaa ctt gaa acc Asp Gln Cys Lys Ser Asp Leu Gln Asn Lys Thr Gln Glu Leu Glu Thr	450	455	460	1394
act caa aaa cat ttg caa gaa act aaa tta caa ctt gtt aaa gaa gaa Thr Gln Lys His Leu Gln Glu Thr Lys Leu Gln Leu Val Lys Glu Glu	465	470	475	1442
tat atc aca tca gct ttg gaa agt act gag gag aaa ctt cat gat gct Tyr Ile Thr Ser Ala Leu Glu Ser Thr Glu Glu Lys Leu His Asp Ala	480	485	490	495
gcc agc aag ctg ctt aac aca gtt gaa gaa act aca aaa gat gta tct Ala Ser Lys Leu Leu Asn Thr Val Glu Glu Thr Thr Lys Asp Val Ser	500	505	510	1538
ggt ctc cat tcc aaa ctg gat cgt aag aag gca gtt gac caa cac aat Gly Leu His Ser Lys Leu Asp Arg Lys Lys Ala Val Asp Gln His Asn	515	520	525	1586
gca gaa gct cag gat att ttt ggc aaa aac ctg aat agt ctg ttt aat Ala Glu Ala Gln Asp Ile Phe Gly Lys Asn Leu Asn Ser Leu Phe Asn	530	535	540	1634
aat atg gaa gaa tta att aag gat ggc agc tca aag caa aag gcc atg Asn Met Glu Glu Leu Ile Lys Asp Gly Ser Ser Lys Gln Lys Ala Met	545	550	555	1682
cta gaa gta cat aag acc tta ttt ggt aat ctg ctg tct tcc agt gtc Leu Glu Val His Lys Thr Leu Phe Gly Asn Leu Leu Ser Ser Ser Val	560	565	570	575
tct gca tta gat acc att act aca gta gca ctt gga tct ctc aca tct Ser Ala Leu Asp Thr Ile Thr Thr Val Ala Leu Gly Ser Leu Thr Ser	580	585	590	1778
att cca gaa aat gtg tct act cat gtt tct cag att ttt aat atg ata				1826

Ile	Pro	Glu	Asn	Val	Ser	Thr	His	Val	Ser	Gln	Ile	Phe	Asn	Met	Ile	
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Leu	Lys	Glu	Gln	Ser	Leu	Ala	Ala	Glu	Ser	Lys	Thr	Val	Leu	Gln	Glu	
		610					615					620				
ttg	att	aat	gta	ctc	aag	act	gat	ctt	cta	agt	tca	ctg	gaa	atg	att	1922
Leu	Ile	Asn	Val	Leu	Lys	Thr	Asp	Leu	Leu	Ser	Ser	Leu	Glu	Met	Ile	
	625					630					635					
tta	tcc	cca	act	gtg	gtg	tct	ata	ctg	aaa	atc	aat	agt	caa	cta	aag	1970
Leu	Ser	Pro	Thr	Val	Val	Ser	Ile	Leu	Lys	Ile	Asn	Ser	Gln	Leu	Lys	
640					645					650					655	
cat	att	ttc	aag	act	tca	ttg	aca	gtg	gcc	gat	aag	ata	gaa	gat	caa	2018
His	Ile	Phe	Lys	Thr	Ser	Leu	Thr	Val	Ala	Asp	Lys	Ile	Glu	Asp	Gln	
				660					665					670		
aaa	aag	gaa	cta	gat	ggc	ttt	ctc	agt	ata	ctg	tgt	aac	aat	cta	cat	2066
Lys	Lys	Glu	Leu	Asp	Gly	Phe	Leu	Ser	Ile	Leu	Cys	Asn	Asn	Leu	His	
			675					680					685			
gaa	cta	caa	gaa	aat	acc	att	tgt	tcc	ttg	gtt	gag	tca	caa	aag	caa	2114
Glu	Leu	Gln	Glu	Asn	Thr	Ile	Cys	Ser	Leu	Val	Glu	Ser	Gln	Lys	Gln	
		690					695					700				
tgt	gga	aac	cta	act	gaa	gac	ctg	aag	aca	ata	aag	cag	acc	cat	tcc	2162
Cys	Gly	Asn	Leu	Thr	Glu	Asp	Leu	Lys	Thr	Ile	Lys	Gln	Thr	His	Ser	
	705					710					715					
cag	gaa	ctt	tgc	aag	tta	atg	aat	ctt	tgg	aca	gag	aga	ttc	tgt	gct	2210
Gln	Glu	Leu	Cys	Lys	Leu	Met	Asn	Leu	Trp	Thr	Glu	Arg	Phe	Cys	Ala	
720						725				730					735	
ttg	gag	gaa	aag	tgt	gaa	aat	ata	cag	aaa	cca	ctt	agt	agt	gtc	cag	2258
Leu	Glu	Glu	Lys	Cys	Glu	Asn	Ile	Gln	Lys	Pro	Leu	Ser	Ser	Val	Gln	
				740					745					750		
gaa	aat	ata	cag	cag	aaa	tct	aag	gat	ata	gtc	aac	aaa	atg	act	ttt	2306
Glu	Asn	Ile	Gln	Gln	Lys	Ser	Lys	Asp	Ile	Val	Asn	Lys	Met	Thr	Phe	
			755					760					765			
cac	agt	caa	aaa	ttt	tgt	gct	gat	tct	gat	ggc	ttc	tca	cag	gaa	ctc	2354
His	Ser	Gln	Lys	Phe	Cys	Ala	Asp	Ser	Asp	Gly	Phe	Ser	Gln	Glu	Leu	
		770					775					780				
aga	aat	ttt	aac	caa	gaa	ggt	aca	aaa	ttg	gtt	gaa	gaa	tct	gtg	aaa	2402
Arg	Asn	Phe	Asn	Gln	Glu	Gly	Thr	Lys	Leu	Val	Glu	Glu	Ser	Val	Lys	
		785				790					795					
cac	tct	gat	aaa	ctc	aat	ggc	aac	ctg	gaa	aaa	ata	tct	caa	gag	act	2450
His	Ser	Asp	Lys	Leu	Asn	Gly	Asn	Leu	Glu	Lys	Ile	Ser	Gln	Glu	Thr	
800					805					810					815	
gaa	cag	aga	tgt	gaa	tct	ctg	aac	aca	aga	aca	gtt	tat	ttt	tct	gaa	2498
Glu	Gln	Arg	Cys	Glu	Ser	Leu	Asn	Thr	Arg	Thr	Val	Tyr	Phe	Ser	Glu	
				820					825					830		
cag	tgg	gta	tct	tcc	tta	aat	gaa	agg	gaa	cag	gaa	ctt	cac	aac	tta	2546
Gln	Trp	Val	Ser	Ser	Leu	Asn	Glu	Arg	Glu	Gln	Glu	Leu	His	Asn	Leu	
			835					840					845			
ttg	gag	gtt	gta	agc	caa	tgt	tgt	gag	gct	tca	agt	tca	gac	atc	act	2594
Leu	Glu	Val	Val	Ser	Gln	Cys	Cys	Glu	Ala	Ser	Ser	Ser	Asp	Ile	Thr	
		850					855					860				

gag aaa tca gat gga dgt aag gca gct cat gag aaa cag cat aac att 2642
 Glu Lys Ser Asp Gly Xaa Lys Ala Ala His Glu Lys Gln His Asn Ile
 865 870 875

ttt ctt gat cag atg act att gat gaa gat aaa ttg ata gca caa aat 2690
 Phe Leu Asp Gln Met Thr Ile Asp Glu Asp Lys Leu Ile Ala Gln Asn
 880 885 890 895

cta gaa ctt aat gaa acc ata aaa att ggt ttg act aag ctt aat tgc 2738
 Leu Glu Leu Asn Glu Thr Ile Lys Ile Gly Leu Thr Lys Leu Asn Cys
 900 905 910

ttt ctg gaa cag gat ctg aaa ctg gat atc cca aca ggt acg aca cca 2786
 Phe Leu Glu Gln Asp Leu Lys Leu Asp Ile Pro Thr Gly Thr Thr Pro
 915 920 925

cag agg aaa agt tat tta tac cca tca aca ctg gta aga act gaa cca 2834
 Gln Arg Lys Ser Tyr Leu Tyr Pro Ser Thr Leu Val Arg Thr Glu Pro
 930 935 940

cgt gaa cat ctc ctt gat cag ctg aaa agg aaa cag cct gag ctg tta 2882
 Arg Glu His Leu Leu Asp Gln Leu Lys Arg Lys Gln Pro Glu Leu Leu
 945 950 955

atg atg cta aac tgt tca gaa aac aac aaa gaa gag aca att ccg gat 2930
 Met Met Leu Asn Cys Ser Glu Asn Asn Lys Glu Glu Thr Ile Pro Asp
 960 965 970 975

gtg gat gta gaa gag gca gtt ctg ggg cag tat act gaa gaa cct cta 2978
 Val Asp Val Glu Glu Ala Val Leu Gly Gln Tyr Thr Glu Glu Pro Leu
 980 985 990

agt caa gag cca tct gta gat gct ggt gtg gat tgt tca tca att ggc 3026
 Ser Gln Glu Pro Ser Val Asp Ala Gly Val Asp Cys Ser Ser Ile Gly
 995 1000 1005

ggg gtt cca ttt ttc cag cat aaa aaa tca cat gga aaa gac aaa gaa 3074
 Gly Val Pro Phe Phe Gln His Lys Lys Ser His Gly Lys Asp Lys Glu
 1010 1015 1020

aac aga ggc att aac aca ctg gag agg tct aaa gtg gaa gaa act aca 3122
 Asn Arg Gly Ile Asn Thr Leu Glu Arg Ser Lys Val Glu Glu Thr Thr
 1025 1030 1035

gag cac ttg gtt aca aag agc aga tta cct ctg cga gcc cag atc aac 3170
 Glu His Leu Val Thr Lys Ser Arg Leu Pro Leu Arg Ala Gln Ile Asn
 1040 1045 1050 1055

ctt taa ttcacttggg ggttggcaat tttattttta aagaaaactt aaaaataaaa 3226
 Leu *

cctgaaaccc cagaacttga gccttgtgta tagattttta aagaatatat atatcagccg 3286
 ggcgcggtgg ctcatgcctg taatcccagc actttgggag gctgaggcgg gtggattgct 3346
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 aatcacttga acccaggaag cggggttgca gtgagccaaa ggtacaccac tacactccag 3526
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 <213> Homo sapiens

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<400> 474

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Arg	Lys	Ala	Ser	Ala	His	Ser	Ile	Val	Glu	Cys	Asp	Pro	Val	Arg	Lys
		35					40				45				
Glu	Val	Ser	Val	Arg	Thr	Gly	Gly	Leu	Ala	Asp	Lys	Ser	Ser	Arg	Lys
	50					55				60					
Thr	Tyr	Thr	Phe	Asp	Met	Val	Phe	Gly	Ala	Ser	Thr	Lys	Gln	Ile	Asp
65					70					75					80
Val	Tyr	Arg	Ser	Val	Val	Cys	Pro	Ile	Leu	Asp	Glu	Val	Ile	Met	Gly
				85					90					95	
Tyr	Asn	Cys	Thr	Ile	Phe	Ala	Tyr	Gly	Gln	Thr	Gly	Thr	Gly	Lys	Thr
			100					105					110		
Phe	Thr	Met	Glu	Gly	Glu	Arg	Ser	Pro	Asn	Glu	Glu	Tyr	Thr	Trp	Glu
		115					120					125			
Glu	Asp	Pro	Leu	Ala	Gly	Ile	Ile	Pro	Arg	Thr	Leu	His	Gln	Ile	Phe
	130					135					140				
Glu	Lys	Leu	Thr	Asp	Asn	Gly	Thr	Glu	Phe	Ser	Val	Lys	Val	Ser	Leu
145					150					155					160
Leu	Glu	Ile	Tyr	Asn	Glu	Glu	Leu	Phe	Asp	Leu	Leu	Asn	Pro	Ser	Ser
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Asp	Val	Ser	Glu	Arg	Leu	Gln	Met	Phe	Asp	Asp	Pro	Arg	Asn	Lys	Arg
			180					185					190		
Gly	Val	Ile	Ile	Lys	Gly	Leu	Glu	Glu	Ile	Thr	Val	His	Asn	Lys	Asp
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Glu	Val	Tyr	Gln	Ile	Leu	Glu	Lys	Gly	Ala	Ala	Lys	Arg	Thr	Thr	Ala
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Ala	Thr	Leu	Met	Asn	Ala	Tyr	Ser	Ser	Arg	Ser	His	Ser	Val	Phe	Ser
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Val	Thr	Ile	His	Met	Lys	Glu	Thr	Thr	Ile	Asp	Gly	Glu	Glu	Leu	Val
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Lys	Ile	Gly	Lys	Leu	Asn	Leu	Val	Asp	Leu	Ala	Gly	Ser	Glu	Asn	Ile
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Gly	Arg	Ser	Gly	Ala	Val	Asp	Lys	Arg	Ala	Arg	Glu	Ala	Gly	Asn	Ile
		275					280					285			
Asn	Gln	Ser	Leu	Leu	Thr	Leu	Gly	Arg	Val	Ile	Thr	Ala	Leu	Val	Glu
	290					295					300				
Arg	Thr	Pro	His	Val	Pro	Tyr	Arg	Glu	Ser	Lys	Leu	Thr	Arg	Ile	Leu
305					310					315					320
Gln	Asp	Ser	Leu	Gly	Gly	Arg	Thr	Arg	Thr	Ser	Ile	Ile	Ala	Thr	Ile
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Ser	Pro	Ala	Ser	Leu	Asn	Leu	Glu	Thr	Leu	Ser	Thr	Leu	Glu	Tyr	
			340				345					350			
Ala	His	Arg	Ala	Lys	Asn	Ile	Leu	Asn	Lys	Pro	Glu	Val	Asn	Gln	Lys
		355					360					365			
Leu	Thr	Lys	Lys	Ala	Leu	Ile	Lys	Glu	Tyr	Thr	Glu	Glu	Ile	Glu	Arg
	370					375					380				
Leu	Lys	Arg	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Asn	Gly	Val	Tyr	Ile	
385					390				395					400	
Ser	Glu	Glu	Asn	Phe	Arg	Val	Met	Ser	Gly	Lys	Leu	Thr	Val	Gln	Glu
			405						410					415	
Glu	Gln	Ile	Val	Glu	Leu	Ile	Glu	Lys	Ile	Gly	Ala	Val	Glu	Glu	Glu
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Leu	Asn	Arg	Val	Thr	Glu	Leu	Phe	Met	Asp	Asn	Lys	Asn	Glu	Leu	Asp
	435						440					445			
Gln	Cys	Lys	Ser	Asp	Leu	Gln	Asn	Lys	Thr	Gln	Glu	Leu	Glu	Thr	Thr
	450					455					460				
Gln	Lys	His	Leu	Gln	Glu	Thr	Lys	Leu	Gln	Leu	Val	Lys	Glu	Glu	Tyr
465					470					475					480
Ile	Thr	Ser	Ala	Leu	Glu	Ser	Thr	Glu	Glu	Lys	Leu	His	Asp	Ala	Ala

Arg Gly Ile Asn Thr Leu Glu Arg Ser Lys Val Glu Glu Thr Thr Glu
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 His Leu Val Thr Lys Ser Arg Leu Pro Leu Arg Ala Gln Ile Asn Leu
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<213> Homo sapiens

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 ccgggccttg attttttggc ggggaccgctc atg gcg tcg cag cca aat tcg tct 114
 Met Ala Ser Gln Pro Asn Ser Ser
 1 5

gcg aag aag aaa gag gag aag ggg aag aac atc cag gtg gtg gtg aga 162
 Ala Lys Lys Lys Glu Glu Lys Gly Lys Asn Ile Gln Val Val Val Arg
 10 15 20

tgc aga cca ttt aat ttg gca gag cgg aaa gct agc gcc cat tca ata 210
 Cys Arg Pro Phe Asn Leu Ala Glu Arg Lys Ala Ser Ala His Ser Ile
 25 30 35 40

gta gaa tgt gat cct gta cga aaa gaa gtt agt gta cga act gga gga 258
 Val Glu Cys Asp Pro Val Arg Lys Glu Val Ser Val Arg Thr Gly Gly
 45 50 55

ttg gct gac aag agc tca agg aaa aca tac act ttt gat atg gtg ttt 306
 Leu Ala Asp Lys Ser Ser Arg Lys Thr Tyr Thr Phe Asp Met Val Phe
 60 65 70

gga gca tct act aaa cag att gat gtt tac cga agt gtt gtt tgt cca 354
 Gly Ala Ser Thr Lys Gln Ile Asp Val Tyr Arg Ser Val Val Cys Pro
 75 80 85

att ctg gat gaa gtt att atg ggc tat aat tgc act atc ttt gcg tat 402
 Ile Leu Asp Glu Val Ile Met Gly Tyr Asn Cys Thr Ile Phe Ala Tyr
 90 95 100

ggc caa act ggc act gga aaa act ttt aca atg gaa ggt gaa agg tca 450
 Gly Gln Thr Gly Thr Gly Lys Thr Phe Thr Met Glu Gly Glu Arg Ser
 105 110 115 120

cct aat gaa gag tat acc tgg gaa gag gat ccc ttg gct ggt ata att 498
 Pro Asn Glu Glu Tyr Thr Trp Glu Glu Asp Pro Leu Ala Gly Ile Ile
 125 130 135

cca cgt acc ctt cat caa att ttt gag aaa ctt act gat aat ggt act 546
 Pro Arg Thr Leu His Gln Ile Phe Glu Lys Leu Thr Asp Asn Gly Thr
 140 145 150

gaa ttt tca gtc aaa gtg tct ctg ttg gag atc tat aat gaa gag ctt 594
 Glu Phe Ser Val Lys Val Ser Leu Leu Glu Ile Tyr Asn Glu Glu Leu
 155 160 165

ttt gat ctt ctt aat cca tca tct gat gtt tct gag aga cta cag atg 642
 Phe Asp Leu Leu Asn Pro Ser Ser Asp Val Ser Glu Arg Leu Gln Met
 170 175 180

ttt gat gat ccc cgt aac aag aga gga gtg ata att aaa ggt tta gaa 690

Phe 185	Asp	Asp	Pro	Arg	Asn 190	Lys	Arg	Gly	Val	Ile 195	Ile	Lys	Gly	Leu	Glu 200	
gaa Glu	att Ile	aca Thr	gta Val	cac His	aac Asn	aag Lys	gat Asp	gaa Glu	gtc Val	tat Tyr	caa Gln	att Ile	tta Leu	gaa Glu	aag Lys	738
ggg Gly	gca Ala	gca Ala	aaa Lys	agg Arg	aca Thr	act Thr	gca Ala	gct Ala	act Thr	ctg Leu	atg Met	aat Asn	gca Ala	tac Tyr	tct Ser	786
agt Ser	cgt Arg	tcc His	cac Ser	tca Val	gtt Phe	ttc Ser	tct Val	gtt Val	aca Thr	ata Ile	cat His	atg Met	aaa Lys	gaa Glu	act Thr	834
acg Thr	att Ile	gat Asp	gga Gly	gaa Glu	gag Glu	ctt Leu	gtt Val	aaa Lys	atc Ile	gga Gly	aag Lys	ttg Leu	aac Asn	ttg Leu	gtt Val	882
gat Asp	ctt Leu	gca Ala	gga Gly	agt Ser	gaa Glu	aac Asn	att Ile	ggc Gly	cgt Arg	tct Ser	gga Gly	gct Ala	gtt Val	gat Asp	aag Lys	930
aga Arg	gct Ala	cgg Arg	gaa Glu	gct Ala	gga Gly	aat Asn	ata Ile	aat Asn	caa Gln	tcc Ser	ctg Leu	ttg Leu	act Thr	ttg Leu	gga Gly	978
agg Arg	gtc Val	att Ile	act Thr	gcc Ala	ctt Leu	gta Val	gaa Glu	aga Arg	aca Thr	cct Pro	cat His	gtt Val	cct Pro	tat Tyr	cga Arg	1026
gaa Glu	tct Ser	aaa Lys	cta Leu	act Thr	aga Arg	atc Ile	ctc Leu	cag Gln	gat Asp	tct Ser	ctt Leu	gga Gly	ggg Gly	cgt Arg	aca Thr	1074
aga Arg	aca Thr	tct Ser	ata Ile	att Ile	gca Ala	aca Thr	att Ile	tct Ser	cct Pro	gca Ala	tct Ser	ctc Leu	aat Asn	ctt Leu	gag Glu	1122
gaa Glu	act Thr	ctg Leu	agt Ser	aca Thr	ttg Leu	gaa Glu	tat Tyr	gct Ala	cat His	aga Arg	gca Ala	aag Lys	aac Asn	ata Ile	ttg Leu	1170
aat Asn	aag Lys	cct Pro	gaa Glu	gtg Val	aat Asn	cag Gln	aaa Lys	ctc Leu	acc Thr	aaa Lys	aaa Lys	gct Ala	ctt Leu	att Ile	aag Lys	1218
gag Glu	tat Tyr	acg Thr	gag Glu	gag Glu	ata Ile	gaa Glu	cgt Arg	tta Leu	aaa Lys	cga Arg	gat Asp	ctt Leu	gct Ala	gca Ala	gcc Ala	1266
cgt Arg	gag Glu	aaa Lys	aat Asn	gga Gly	gtg Val	tat Tyr	att Ile	tct Ser	gaa Glu	gaa Glu	aat Asn	ttt Phe	aga Arg	gtc Val	atg Met	1314
agt Ser	gga Gly	aaa Lys	tta Leu	act Thr	gtt Val	caa Gln	gaa Glu	gag Glu	cag Gln	att Ile	gta Val	gaa Glu	ttg Leu	att Ile	gaa Glu	1362
aaa Lys	att Ile	ggt Gly	gct Ala	gtt Val	gag Glu	gag Glu	gag Glu	ctg Leu	aat Asn	agg Arg	gtt Val	aca Thr	gag Glu	ttg Leu	ttt Phe	1410
atg Met	gat Asp	aat Asn	aaa Lys	aat Asn	gaa Glu	ctt Leu	gac Asp	cag Gln	tgt Cys	aaa Lys	tct Ser	gac Asp	ctg Leu	caa Gln	aat Asn	1458

aaa aca caa gaa ctt gaa acc act caa aaa cat ttg caa gaa act aaa	1506
Lys Thr Gln Glu Leu Glu Thr Thr Gln Lys His Leu Gln Glu Thr Lys	
460 465 470	
tta caa ctt gtt aaa gaa gaa tat atc aca tca gct ttg gaa agt act	1554
Leu Gln Leu Val Lys Glu Glu Tyr Ile Thr Ser Ala Leu Glu Ser Thr	
475 480 485	
gag gag aaa ctt cat gat gct gcc agc aag ctg ctt aac aca gtt gaa	1602
Glu Glu Lys Leu His Asp Ala Ala Ser Lys Leu Leu Asn Thr Val Glu	
490 495 500	
gaa act aca aaa gat gta tct ggt ctc cat tcc aaa ctg gat cgt aag	1650
Glu Thr Thr Lys Asp Val Ser Gly Leu His Ser Lys Leu Asp Arg Lys	
505 510 515 520	
aag gca gtt gac caa cac aat gca gaa gct cag gat att ttt ggc aaa	1698
Lys Ala Val Asp Gln His Asn Ala Glu Ala Gln Asp Ile Phe Gly Lys	
525 530 535	
aac ctg aat agt ctg ttt aat aat atg gaa gaa tta att aag gat ggc	1746
Asn Leu Asn Ser Leu Phe Asn Asn Met Glu Glu Leu Ile Lys Asp Gly	
540 545 550	
agc tca aag caa aag gcc atg cta gaa gta cat aag acc tta ttt ggt	1794
Ser Ser Lys Gln Lys Ala Met Leu Glu Val His Lys Thr Leu Phe Gly	
555 560 565	
aat ctg ctg tct tcc agt gtc tct gca tta gat acc att act aca gta	1842
Asn Leu Leu Ser Ser Ser Val Ser Ala Leu Asp Thr Ile Thr Thr Val	
570 575 580	
gca ctt gga tct ctc aca tct att cca gaa aat gtg tct act cat gtt	1890
Ala Leu Gly Ser Leu Thr Ser Ile Pro Glu Asn Val Ser Thr His Val	
585 590 595 600	
tct cag att ttt aat atg ata cta aaa gaa caa tca tta gca gca gaa	1938
Ser Gln Ile Phe Asn Met Ile Leu Lys Glu Gln Ser Leu Ala Ala Glu	
605 610 615	
agt aaa act gta cta cag gaa ttg att aat gta ctc aag act gat ctt	1986
Ser Lys Thr Val Leu Gln Glu Leu Ile Asn Val Leu Lys Thr Asp Leu	
620 625 630	
cta agt tca ctg gaa atg att tta tcc cca act gtg gtg tct ata ctg	2034
Leu Ser Ser Leu Glu Met Ile Leu Ser Pro Thr Val Val Ser Ile Leu	
635 640 645	
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Lys Ile Asn Ser Gln Leu Lys His Ile Phe Lys Thr Ser Leu Thr Val	
650 655 660	
gcc gat aag ata gaa gat caa aaa aag gaa cta gat ggc ttt ctc agt	2130
Ala Asp Lys Ile Glu Asp Gln Lys Lys Glu Leu Asp Gly Phe Leu Ser	
665 670 675 680	
ata ctg tgt aac aat cta cat gaa cta caa gaa aat acc att tgt tcc	2178
Ile Leu Cys Asn Asn Leu His Glu Leu Gln Glu Asn Thr Ile Cys Ser	
685 690 695	
ttg gtt gag tca caa aag caa tgt gga aac cta act gaa gac ctg aag	2226
Leu Val Glu Ser Gln Lys Gln Cys Gly Asn Leu Thr Glu Asp Leu Lys	
700 705 710	
aca ata aag cag acc cat tcc cag gaa ctt tgc aag tta atg aat ctt	2274
Thr Ile Lys Gln Thr His Ser Gln Glu Leu Cys Lys Leu Met Asn Leu	
715 720 725	

tgg aca gag aga ttc tgt gct ttg gag gaa aag tgt gaa aat ata cag	2322
Trp Thr Glu Arg Phe Cys Ala Leu Glu Glu Lys Cys Glu Asn Ile Gln	
730 735 740	
aaa cca ctt agt agt gtc cag gaa aat ata cag cag aaa tct aag gat	2370
Lys Pro Leu Ser Ser Val Gln Glu Asn Ile Gln Gln Lys Ser Lys Asp	
745 750 755 760	
ata gtc aac aaa atg act ttt cac agt caa aaa ttt tgt gct gat tct	2418
Ile Val Asn Lys Met Thr Phe His Ser Gln Lys Phe Cys Ala Asp Ser	
765 770 775	
gat ggc ttc tca cag gaa ctc aga aat ttt aac caa gaa ggt aca aaa	2466
Asp Gly Phe Ser Gln Glu Leu Arg Asn Phe Asn Gln Glu Gly Thr Lys	
780 785 790	
ttg gtt gaa gaa tct gtg aaa cac tct gat aaa ctc aat ggc aac ctg	2514
Leu Val Glu Glu Ser Val Lys His Ser Asp Lys Leu Asn Gly Asn Leu	
795 800 805	
gaa aaa ata tct caa gag act gaa cag aga tgt gaa tct ctg aac aca	2562
Glu Lys Ile Ser Gln Glu Thr Gln Arg Cys Glu Ser Leu Asn Thr	
810 815 820	
aga aca gtt tat ttt tct gaa cag tgg gta tct tcc tta aat gaa agg	2610
Arg Thr Val Tyr Phe Ser Glu Gln Trp Val Ser Ser Leu Asn Glu Arg	
825 830 835 840	
gaa cag gaa ctt cac aac tta ttg gag gtt gta agc caa tgt tgt gag	2658
Glu Gln Glu Leu His Asn Leu Leu Glu Val Val Ser Gln Cys Cys Glu	
845 850 855	
gct tca agt tca gac atc act gag aaa tca gat gga dgt aag gca gct	2706
Ala Ser Ser Ser Asp Ile Thr Glu Lys Ser Asp Gly Xaa Lys Ala Ala	
860 865 870	
cat gag aaa cag cat aac att ttt ctt gat cag atg act att gat gaa	2754
His Glu Lys Gln His Asn Ile Phe Leu Asp Gln Met Thr Ile Asp Glu	
875 880 885	
gat aaa ttg ata gca caa aat cta gaa ctt aat gaa acc ata aaa att	2802
Asp Lys Leu Ile Ala Gln Asn Leu Glu Leu Asn Glu Thr Ile Lys Ile	
890 895 900	
ggt ttg act aag ctt aat tgc ttt ctg gaa cag gat ctg aaa ctg gat	2850
Gly Leu Thr Lys Leu Asn Cys Phe Leu Glu Gln Asp Leu Lys Leu Asp	
905 910 915 920	
atc cca aca ggt acg aca cca cag agg aaa agt tat tta tac cca tca	2898
Ile Pro Thr Gly Thr Thr Pro Gln Arg Lys Ser Tyr Leu Tyr Pro Ser	
925 930 935	
aca ctg gta aga act gaa cca cgt gaa cat ctc ctt gat cag ctg aaa	2946
Thr Leu Val Arg Thr Glu Pro Arg Glu His Leu Leu Asp Gln Leu Lys	
940 945 950	
agg aaa cag cct gag ctg tta atg atg cta aac tgt tca gaa aac aac	2994
Arg Lys Gln Pro Glu Leu Leu Met Met Leu Asn Cys Ser Glu Asn Asn	
955 960 965	
aaa gaa gag aca att ccg gat gtg gat gta gaa gag gca gtt ctg ggg	3042
Lys Glu Glu Thr Ile Pro Asp Val Asp Val Glu Glu Ala Val Leu Gly	
970 975 980	
cag tat act gaa gaa cct cta agt caa gag cca tct gta gat gct ggt	3090
Gln Tyr Thr Glu Glu Pro Leu Ser Gln Glu Pro Ser Val Asp Ala Gly	

985	990	995	1000	
gtg gat tgt tca tca att ggc ggg gtt cca ttt ttc cag cat aaa aaa				3138
Val Asp Cys Ser Ser Ile Gly Gly Val Pro Phe Phe Gln His Lys Lys				
1005	1010	1015		
tca cat gga aaa gac aaa gaa aac aga ggc att aac aca ctg gag agg				3186
Ser His Gly Lys Asp Lys Glu Asn Arg Gly Ile Asn Thr Leu Glu Arg				
1020	1025	1030		
tct aaa gtg gaa gaa act aca gag cac ttg gtt aca aag agc aga tta				3234
Ser Lys Val Glu Glu Thr Thr Glu His Leu Val Thr Lys Ser Arg Leu				
1035	1040	1045		
cct ctg cga gcc cag atc aac ctt taa ttcacttgagg ggttggaat				3281
Pro Leu Arg Ala Gln Ile Asn Leu *				
1050	1055			
tttatttttta aagaaaactt aaaaataaaa cctgaaaccc cagaacttga gccttggtga				3341
tagattttta aagaatatat atatcagccg ggcgcggtgg ctcatgcctg taateccagc				3401
actttgggag gctgagggcg gtggattgct tgagcccagg agtttgagac cagcctggcc				3461
aacgtggcaa aacctcgtct ctgttaaaaa ttagccgggc gtggtggcac actcctgtaa				3521
tcccagctac tggggaggct gaggcacgag aatcacttga acccaggaag cgggggttga				3581
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gtatcttttt ctcgattcaa atcttaaccc ttaggactct ggtatttttg atctggcaac				4541
catatttctg gaagttgaga tgtttcagct tgaagaacca aaacagaagg aatatgtaca				4601
aagaataaat tttctgctca cgatgagttt agtgtgtaaa gtttagagac atctgacttt				4661
gatagctaaa ttaaaccaaa ccctattgaa gaattgaata tatgtactt caagaaacta				4721
aattgatctc gtagaattat cttaataaaa taatggctat aatttctctg caaaatcaga				4781
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aatgtggttt ctacatt				4858

<210> 476
 <211> 1056
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> 869
 <223> Xaa = Any Amino Acid

<400> 476
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 Arg Lys Ala Ser Ala His Ser Ile Val Glu Cys Asp Pro Val Arg Lys
 35 40 45
 Glu Val Ser Val Arg Thr Gly Gly Leu Ala Asp Lys Ser Ser Arg Lys
 50 55 60
 Thr Tyr Thr Phe Asp Met Val Phe Gly Ala Ser Thr Lys Gln Ile Asp
 65 70 75 80

Val	Tyr	Arg	Ser	Val	Val	Cys	Pro	Ile	Leu	Asp	Glu	Val	Ile	Met	Gly
				85					90					95	
Tyr	Asn	Cys	Thr	Ile	Phe	Ala	Tyr	Gly	Gln	Thr	Gly	Thr	Gly	Lys	Thr
				100				105					110		
Phe	Thr	Met	Glu	Gly	Glu	Arg	Ser	Pro	Asn	Glu	Glu	Tyr	Thr	Trp	Glu
		115					120					125			
Glu	Asp	Pro	Leu	Ala	Gly	Ile	Ile	Pro	Arg	Thr	Leu	His	Gln	Ile	Phe
	130					135					140				
Glu	Lys	Leu	Thr	Asp	Asn	Gly	Thr	Glu	Phe	Ser	Val	Lys	Val	Ser	Leu
145					150					155					160
Leu	Glu	Ile	Tyr	Asn	Glu	Glu	Leu	Phe	Asp	Leu	Leu	Asn	Pro	Ser	Ser
				165					170					175	
Asp	Val	Ser	Glu	Arg	Leu	Gln	Met	Phe	Asp	Asp	Pro	Arg	Asn	Lys	Arg
			180					185					190		
Gly	Val	Ile	Ile	Lys	Gly	Leu	Glu	Glu	Ile	Thr	Val	His	Asn	Lys	Asp
		195					200					205			
Glu	Val	Tyr	Gln	Ile	Leu	Glu	Lys	Gly	Ala	Ala	Lys	Arg	Thr	Thr	Ala
	210					215						220			
Ala	Thr	Leu	Met	Asn	Ala	Tyr	Ser	Ser	Arg	Ser	His	Ser	Val	Phe	Ser
225				230						235					240
Val	Thr	Ile	His	Met	Lys	Glu	Thr	Thr	Ile	Asp	Gly	Glu	Glu	Leu	Val
				245					250					255	
Lys	Ile	Gly	Lys	Leu	Asn	Leu	Val	Asp	Leu	Ala	Gly	Ser	Glu	Asn	Ile
			260					265					270		
Gly	Arg	Ser	Gly	Ala	Val	Asp	Lys	Arg	Ala	Arg	Glu	Ala	Gly	Asn	Ile
		275					280					285			
Asn	Gln	Ser	Leu	Leu	Thr	Leu	Gly	Arg	Val	Ile	Thr	Ala	Leu	Val	Glu
	290					295					300				
Arg	Thr	Pro	His	Val	Pro	Tyr	Arg	Glu	Ser	Lys	Leu	Thr	Arg	Ile	Leu
305				310						315					320
Gln	Asp	Ser	Leu	Gly	Gly	Arg	Thr	Arg	Thr	Ser	Ile	Ile	Ala	Thr	Ile
				325					330					335	
Ser	Pro	Ala	Ser	Leu	Asn	Leu	Glu	Glu	Thr	Leu	Ser	Thr	Leu	Glu	Tyr
			340					345					350		
Ala	His	Arg	Ala	Lys	Asn	Ile	Leu	Asn	Lys	Pro	Glu	Val	Asn	Gln	Lys
		355					360					365			
Leu	Thr	Lys	Lys	Ala	Leu	Ile	Lys	Glu	Tyr	Thr	Glu	Glu	Ile	Glu	Arg
	370					375					380				
Leu	Lys	Arg	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Asn	Gly	Val	Tyr	Ile	
385				390					395					400	
Ser	Glu	Glu	Asn	Phe	Arg	Val	Met	Ser	Gly	Lys	Leu	Thr	Val	Gln	Glu
			405						410					415	
Glu	Gln	Ile	Val	Glu	Leu	Ile	Glu	Lys	Ile	Gly	Ala	Val	Glu	Glu	Glu
			420					425					430		
Leu	Asn	Arg	Val	Thr	Glu	Leu	Phe	Met	Asp	Asn	Lys	Asn	Glu	Leu	Asp
		435					440					445			
Gln	Cys	Lys	Ser	Asp	Leu	Gln	Asn	Lys	Thr	Gln	Glu	Leu	Glu	Thr	Thr
	450					455					460				
Gln	Lys	His	Leu	Gln	Glu	Thr	Lys	Leu	Gln	Leu	Val	Lys	Glu	Glu	Tyr
465				470					475					480	
Ile	Thr	Ser	Ala	Leu	Glu	Ser	Thr	Glu	Glu	Lys	Leu	His	Asp	Ala	Ala
			485						490				495		
Ser	Lys	Leu	Leu	Asn	Thr	Val	Glu	Glu	Thr	Thr	Lys	Asp	Val	Ser	Gly
			500					505					510		
Leu	His	Ser	Lys	Leu	Asp	Arg	Lys	Lys	Ala	Val	Asp	Gln	His	Asn	Ala
		515					520					525			
Glu	Ala	Gln	Asp	Ile	Phe	Gly	Lys	Asn	Leu	Asn	Ser	Leu	Phe	Asn	Asn
	530					535					540				
Met	Glu	Glu	Leu	Ile	Lys	Asp	Gly	Ser	Ser	Lys	Gln	Lys	Ala	Met	Leu
545				550						555					560
Glu	Val	His	Lys	Thr	Leu	Phe	Gly	Asn	Leu	Leu	Ser	Ser	Ser	Val	Ser
			565						570					575	
Ala	Leu	Asp	Thr	Ile	Thr	Thr	Val	Ala	Leu	Gly	Ser	Leu	Thr	Ser	Ile
			580					585					590		
Pro	Glu	Asn	Val	Ser	Thr	His	Val	Ser	Gln	Ile	Phe	Asn	Met	Ile	Leu
		595					600					605			
Lys	Glu	Gln	Ser	Leu	Ala	Ala	Glu	Ser	Lys	Thr	Val	Leu	Gln	Glu	Leu

610	Ile Asn Val Leu Lys Thr Asp Leu Leu Ser Ser Leu Glu Met Ile Leu	615	620
625	Ser Pro Thr Val Val Ser Ile Leu Lys Ile Asn Ser Gln Leu Lys His	630	635
	645	650	655
Ile Phe Lys Thr Ser Leu Thr Val Ala Asp Lys Ile Glu Asp Gln Lys	660	665	670
Lys Glu Leu Asp Gly Phe Leu Ser Ile Leu Cys Asn Asn Leu His Glu	675	680	685
Leu Gln Glu Asn Thr Ile Cys Ser Leu Val Glu Ser Gln Lys Gln Cys	690	695	700
Gly Asn Leu Thr Glu Asp Leu Lys Thr Ile Lys Gln Thr His Ser Gln	705	710	715
Glu Leu Cys Lys Leu Met Asn Leu Trp Thr Glu Arg Phe Cys Ala Leu	725	730	735
Glu Glu Lys Cys Glu Asn Ile Gln Lys Pro Leu Ser Ser Val Gln Glu	740	745	750
Asn Ile Gln Gln Lys Ser Lys Asp Ile Val Asn Lys Met Thr Phe His	755	760	765
Ser Gln Lys Phe Cys Ala Asp Ser Asp Gly Phe Ser Gln Glu Leu Arg	770	775	780
Asn Phe Asn Gln Glu Gly Thr Lys Leu Val Glu Glu Ser Val Lys His	785	790	795
Ser Asp Lys Leu Asn Gly Asn Leu Glu Lys Ile Ser Gln Glu Thr Glu	805	810	815
Gln Arg Cys Glu Ser Leu Asn Thr Arg Thr Val Tyr Phe Ser Glu Gln	820	825	830
Trp Val Ser Ser Leu Asn Glu Arg Glu Gln Glu Leu His Asn Leu Leu	835	840	845
Glu Val Val Ser Gln Cys Cys Glu Ala Ser Ser Ser Asp Ile Thr Glu	850	855	860
Lys Ser Asp Gly Xaa Lys Ala Ala His Glu Lys Gln His Asn Ile Phe	865	870	875
Leu Asp Gln Met Thr Ile Asp Glu Asp Lys Leu Ile Ala Gln Asn Leu	885	890	895
Glu Leu Asn Glu Thr Ile Lys Ile Gly Leu Thr Lys Leu Asn Cys Phe	900	905	910
Leu Glu Gln Asp Leu Lys Leu Asp Ile Pro Thr Gly Thr Thr Pro Gln	915	920	925
Arg Lys Ser Tyr Leu Tyr Pro Ser Thr Leu Val Arg Thr Glu Pro Arg	930	935	940
Glu His Leu Leu Asp Gln Leu Lys Arg Lys Gln Pro Glu Leu Leu Met	945	950	955
Met Leu Asn Cys Ser Glu Asn Asn Lys Glu Glu Thr Ile Pro Asp Val	965	970	975
Asp Val Glu Glu Ala Val Leu Gly Gln Tyr Thr Glu Glu Pro Leu Ser	980	985	990
Gln Glu Pro Ser Val Asp Ala Gly Val Asp Cys Ser Ser Ile Gly Gly	995	1000	1005
Val Pro Phe Phe Gln His Lys Lys Ser His Gly Lys Asp Lys Glu Asn	1010	1015	1020
Arg Gly Ile Asn Thr Leu Glu Arg Ser Lys Val Glu Glu Thr Thr Glu	1025	1030	1035
His Leu Val Thr Lys Ser Arg Leu Pro Leu Arg Ala Gln Ile Asn Leu	1045	1050	1055

<210> 477
 <211> 919
 <212> DNA
 <213> Homo sapiens

<220>
 <221> allele
 <222> 420
 <223> N is any

<400> 477

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caagggattg	gaattgagga	agactgttac	tacagttgag	actcagaact	tggaaggcct	180
gcatcatgat	ggccaattct	gccataahcc	ctgtcctcca	gatgtgaaca	tggaatcatc	240
aaggaatgca	cactcaccag	caacaccaag	tgcaaagagg	aaggatccag	atctaacttg	300
gggtggtctt	gtcttcttct	tttgccaatt	ccactaattg	tttgggtgaa	gagaaaggaa	360
gtacagaaaa	catgcagaaa	gcacagaaaag	gaaaaccaag	gttctcatga	atctccaacn	420
ttaaatcctg	aaacagtggc	aataaatttt	cagatgttga	cttgagtaaa	tatatcacca	480
ctattgctgg	agtcatgaca	ctaagtcaag	ttaaaggctt	tggtcgaaaag	aatggtgtca	540
atgaagccaa	aatagatgag	atcaagaatg	acaatgtcca	agacacagca	gaacagaaaag	600
ttcaactgct	tcgtaattgg	catcaacttc	atggaaagaa	agaagcgtat	gacacattga	660
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tcaaggacat	tactagtgc	tcagaaaatt	caaacttcag	aaatgaaatc	caaagcttgg	780
tctagagtg	aaaacaacaa	attcagttct	gagtatatgc	aattagtggt	tgaaaagatt	840
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gcgctgaaga	gccaacata					919

<210> 478

<211> 2533

<212> DNA

<213> Homo sapiens

<220>

<221> allele

<222> 416,836,1766

<223> N is any

<400> 478

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ctcccgcggg	ttggtggacc	cgctcagtac	ggagttgggg	aagctctttc	acttcggagg	180
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aattgaggaa	cagctgttact	acagttgaga	ctcagaactt	ggaaggcctg	catcatgatg	360
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aaataaactg	caccgcggacc	cagaatacca	agtgacagatg	taaaccaaac	tttttttcta	600
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gaaagtttgt	attaaatgtg	aattttaaga	aataatattt	atatttctgt	aaatgtaaac	2400
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<210> 479
 <211> 2550
 <212> DNA
 <213> Homo sapiens

<220>
 <221> allele
 <222> 442,862,1792
 <223> n is any

<400> 479					
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tggctgcccc	ggcggagctg	cctcttctcc	cgcggttggg	tggacccgct	cagtacggag 180
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<220>

<221> allele
 <222> 247,604
 <223> N is any

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 <213> Homo sapiens

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<211> 6012

<212> DNA

<213> Homo sapiens

<400> 483

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<211> 202100

<212> DNA

<213> Homo sapiens

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Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Xaa Lys Glu Asp Tyr Ile 235			
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Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met 250			
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Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp 265			
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Thr Leu Ala His His Xaa Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys 280			
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Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu 300			
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Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr 315			
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Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu 330			
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Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro 345			
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His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp 360			
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ccc can tgg aaa aca gat tcc tgc cag gga gac tca ggg gga ccc ctc 1216			
Pro Xaa Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu 380			
365	370	375	
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Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp
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 Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val
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